c) subjecting said libraries to affinity or functional selection steps to generate artificial SH3 domains.

2. (amended) The method according to claim 1, wherein step a) comprises replacing amino acid residues in a variable region of the RT-loop with a random combination of any other amino acid residues.

3. (amended) The method according to claim 2, wherein the amino acid residues in the variable region of the RT-loop that are replaced comprise six amino acid residues that immediately follow a conserved stretch of amino acids having an ALYDY (SEQ ID NO:1) consensus sequence.

4. (amended) The method according to claim 1, wherein the recombinant libraries comprise said RRT-SH3 domains in plasmid, phagemid or viral vectors.

Please add the following new claims 17-19.

--17. The method according to claim 3, wherein the six amino acids that are replaced in the RT-loop are replaced with a peptide motif selected from the group consisting of XSWSXX (SEQ ID NO:28), XSPFXX (SEQ ID NO:30) and XSXFPW (SEQ ID NO:32), wherein X is any amino acid.

18. The method of claim 17, wherein X is an amino acid selected from the group consisting of V, F, D, M, P, S, T, W, and Y (SEQ ID NOS:29 and 30).

19. The method of claim 17, wherein the peptide motif is selected from the group consisting of VSWSPD (SEQ ID NO:6), FSWSDT (SEQ ID NO:7), DSWSTS (SEQ ID NO:8), YSWSDM (SEQ ID NO:9), WSPFPS (SEQ ID NO:10), DSPFSF (SEQ ID NO:11), FSPFSF (SEQ ID NO:12), FSPFDW (SEQ ID NO:13), SSPFDW (SEQ ID NO:14), YSPFSW (SEQ ID NO:15), TSPFPW (SEQ ID NO:16), YSFFPW (SEQ ID NO:17), YSDFPW (SEQ ID NO:18) and DSWFPW (SEQ ID NO:19).--